MS11-P04

The crystal structure of the CARD-CARD disk of the human apoptosome and its structural insights into the assembly of the death-domain fold

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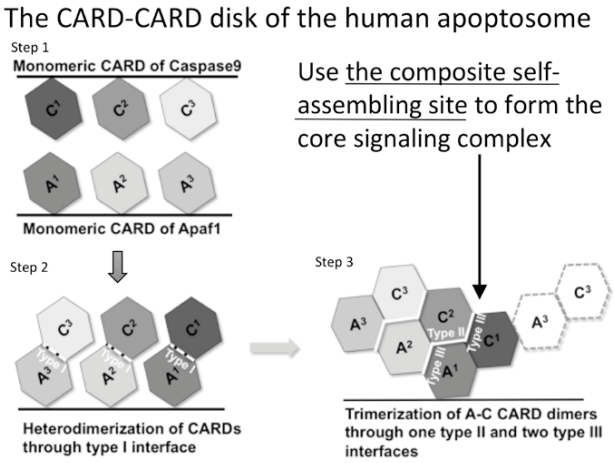
The caspase recruitment domain (CARD) of the human apoptosome recruits caspase-9 CARD via the homotypic interactions for caspase activation in apoptosis. Here we present the crystal structure of the CARD-CARD disk of the human apoptosome and also show the difference in the CARD assembly between the *Caenorhabditis elegans*, Drosophila, and human apoptosomes, which suggests that the helical assembly only exists in the vertabtate DD-folds. We also found that of the death-domain folds have five different assembling mechanisms for their specific roles in signal transduction.



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Keywords: Apoptosome, assembly, death domain

MS11-P05

Structure of human natural killer cell receptor NKR-P1 in complex with its ligand LLT1

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Natural killer cells are white blood cells able to kill tumor, virus-infected or stressed cells. NKR-P1 is a C-type lectin like-receptor on surface of human natural killer cells and LLT1 is its binding partner belonging to the same structural family.

Recently, we have expressed, purified and solved four crystal structures of the extracellular part of LLT1 in monomeric, dimeric and hexameric form [1, 2]. In this contribution, we present three more structures characterizing this receptor-ligand binding pair: structures of the extracellular part of NKR-P1 in the fully glycosylated and deglycosylated form and a structure of the NKR-P1:LLT1 complex. Expression and purification of NKR-P1 was described by us recently as well [3].

All three crystal structures show NKR-P1 in a dimeric form with an unexpected dimerization mode. Unlike LLT1, which has the α2 helix in the dimerization interface, NKR-P1 dimer has the α1 helix in its dimerization interface. This different dimeric arrangement of both proteins enables spatial connection of NKR-P1 with LLT1 not only in a single molecular complex, but in a periodical chain of alternating receptor/ligand molecules. Such chain we really observe in the presented crystal structure.

Acknowledgement: This study was supported by BIOCEV (ERDF CZ.1.05/1.1.00/02.0109), Czech Science Foundation (15-15181S and 18-10687S), MEYS of the Czech Republic (LTC17065 within the COST Action CA15126), Charles University (UNCE 204025/2012, GAUK 161216), and Instruct (R&D pilot scheme APPID 56 and 286).

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Keywords: immune receptor, natural killer cell, protein-protein complex